

10000187.061302



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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,187

DATE: 07/15/2002

TIME: 12:38:09

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Output Set: N:\CRF3\07152002\J049187.raw

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3 <110> APPLICANT: CHOI, YANG-DO
4     CHEONG, JONG-JOO
5     LEE, JONG-SEOB
6     SONG, JONG-TAE
7     SONG, SANG-IK
8     SEO, HAK-SOO
9     KOO, YEON-JONG
11 <120> TITLE OF INVENTION: GENES FOR S-ADENOSYL L-METHIONINE: JASMONIC ACID
12     CARBOXYL METHYLTRANSFERASE AND A METHOD FOR THE
13     DEVELOPMENT OF PATHOGEN- AND STRESS-RESISTANT PLANTS
14     USING THE GENES
16 <130> FILE REFERENCE: 058333/0112
18 <140> CURRENT APPLICATION NUMBER: 10/049,187
C--> 19 <141> CURRENT FILING DATE: 2002-06-13
21 <150> PRIOR APPLICATION NUMBER: PCT/KR01/00953
22 <151> PRIOR FILING DATE: 2001-06-05
24 <160> NUMBER OF SEQ ID NOS: 8
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1170
30 <212> TYPE: DNA
31 <213> ORGANISM: Arabidopsis thaliana
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35 aactccaccg ctcagagcaa cataatatct ctaggcagaa gagtaatgga cgaggccttg 120
36 aagaagttaa tgatgagcaa ttcagagatt tcgagcattg gaatcgccga cttaggctgc 180
37 tcctccggtc cgaacagtct cttgtccatc tccaacatag ttgacacgat ccacaacttg 240
38 tgtcctgacc tcgaccgtcc agtccctgag ctgagagtct ctctcaacga cctccctagc 300
39 aatgacttca actacatatg tgcttctttg ccagagtttt acgaccgggt taataataac 360
40 aaggagggtt taggggttcgg tcgtggagga ggagaatcgt gttttgtgtc ggccgtccca 420
41 ggttcggttc acggacgttt gtttcctcgc cggagccttc actttgtgca ttcttcttct 480
42 agttttacatt ggttgtctca ggttccatgt cgtgaggcgg agaaggaaga caggacaata 540
43 acagctgatt tagaaaacat ggggaaaata tacatatcaa agacaagtcc taagagtgc 600
44 cataaagctt atgctcttca attccaaact gatttcttgg tttttttgag gtcacgatct 660
45 gaggagttgg tcccgggagg ccgaatggtt ttatcggttc ttggtagaag atcactggat 720
46 cccacaaccg aagagagttg ctatcaatgg gaactcctag ctcaagctct tatgtccatg 780
47 gccaaagagg gtatcatcga ggaagagaag atcgatgctt tcaacgctcc ttactatgct 840
48 gcgagctccg aagagttgaa aatgggtgata gagaaagaag ggtcattttc gatcgatagg 900
49 cttgagataa gtccgattga ttgggaaggt gggagtatca gtgaggagag ttatgacctt 960
50 gcaataaggt ccaaaccgga agccctagct agtggccgaa gagtgtctaa taccataaga 1020
51 gctgtggtcg agccgatgct agaacctact ttccggtgaa atgtgatgga cgagcttttt 1080
52 gaaaggtatg caaagatcgt gggagagtac ttctatgtaa gctcgccacg atacgctatt 1140
53 gttattcttt cgctcgttag aaccggttag

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58 <212> TYPE: DNA
59 <213> ORGANISM: Arabidopsis thaliana
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62 <221> NAME/KEY: CDS
63 <222> LOCATION: (15)..(1181)
64 <223> OTHER INFORMATION: open reading frame for JMT
66 <400> SEQUENCE: 2
67 aaagagagag agag atg gag gta atg cga gtt ctt cac atg aac aaa gga 50
68 Met Glu Val Met Arg Val Leu His Met Asn Lys Gly
69 1 5 10
71 aac ggg gaa aca agt tat gcc aag aac tcc acc gct cag agc aac ata 98
72 Asn Gly Glu Thr Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile
73 15 20 25
75 ata tct cta ggc aga aga gta atg gac gag gcc ttg aag aag tta atg 146
76 Ile Ser Leu Gly Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met
77 30 35 40
79 atg agc aat tca gag att tcg agc att gga atc gcc gac tta ggc tgc 194
80 Met Ser Asn Ser Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys
81 45 50 55 60
83 tcc tcc ggt ccg aac agt ctc ttg tcc atc tcc aac ata gtt gac acg 242
84 Ser Ser Gly Pro Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr
85 65 70 75
87 atc cac aac ttg tgt cct gac ctc gac cgt cca gtc cct gag ctc aga 290
88 Ile His Asn Leu Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg
89 80 85 90
91 gtc tct ctc aac gac ctc cct agc aat gac ttc aac tac ata tgt gct 338
92 Val Ser Leu Asn Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala
93 95 100 105
95 tct ttg cca gag ttt tac gac cgg gtt aat aat aac aag gag ggt tta 386
96 Ser Leu Pro Glu Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu
97 110 115 120
99 ggg ttc ggt cgt gga gga gga gaa tcg tgt ttt gtg tcg gcc gtc cca 434
100 Gly Phe Gly Arg Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro
101 125 130 135 140
103 ggt tcg ttc tac gga cgt ttg ttt cct cgc cgg agc ctt cac ttt gtg 482
104 Gly Ser Phe Tyr Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val
105 145 150 155
107 cat tct tct tct agt tta cat tgg ttg tct cag gtt cca tgt cgt gag 530
108 His Ser Ser Ser Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu
109 160 165 170
111 gcg gag aag gaa gac agg aca ata aca gct gat tta gaa aac atg ggg 578
112 Ala Glu Lys Glu Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly
113 175 180 185
115 aaa ata tac ata tca aag aca agt cct aag agt gca cat aaa gct tat 626
116 Lys Ile Tyr Ile Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr
117 190 195 200
119 gct ctt caa ttc caa act gat ttc ttg gtt ttt ttg agg tca cga tct 674

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120 Ala Leu Gln Phe Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser
121 205                210                215                220
123 gag gag ttg gtc ccg gga ggc cga atg gtt tta tcg ttc ctt ggt aga 722
124 Glu Glu Leu Val Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg
125                225                230                235
127 aga tca ctg gat ccc aca acc gaa gag agt tgc tat caa tgg gaa ctc 770
128 Arg Ser Leu Asp Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu
129                240                245                250
131 cta gct caa gct ctt atg tcc atg gcc aaa gag ggt atc atc gag gaa 818
132 Leu Ala Gln Ala Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu
133                255                260                265
135 gag aag atc gat gct ttc aac gct cct tac tat gct gcg agc tcc gaa 866
136 Glu Lys Ile Asp Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu
137                270                275                280
139 gag ttg aaa atg gtg ata gag aaa gaa ggg tca ttt tcg atc gat agg 914
140 Glu Leu Lys Met Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg
141 285                290                295                300
143 ctt gag ata agt ccg att gat tgg gaa ggt ggg agt atc agt gag gag 962
144 Leu Glu Ile Ser Pro Ile Asp Trp Glu Gly Ser Ile Ser Glu Glu
145                305                310                315
147 agt tat gac ctt gca ata agg tcc aaa ccc gaa gcc cta gct agt ggc 1010
148 Ser Tyr Asp Leu Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly
149                320                325                330
151 cga aga gtg tct aat acc ata aga gct gtg gtc gag ccg atg cta gaa 1058
152 Arg Arg Val Ser Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu
153                335                340                345
155 cct act ttc ggt gaa aat gtg atg gac gag ctt ttt gaa agg tat gca 1106
156 Pro Thr Phe Gly Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala
157                350                355                360
159 aag atc gtg gga gag tac ttc tat gta agc tcg cca cga tac gct att 1154
160 Lys Ile Val Gly Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile
161 365                370                375                380
163 gtt att ctt tcg ctc gtt aga acc ggt tgatcgtgtt ataacatatg 1201
164 Val Ile Leu Ser Leu Val Arg Thr Gly
165                385
167 ccaatataca tgtcttttggg cctacaatga catgatttgg tagtttttcta atcaagcata 1261
169 tgtaatatataa tttgcttcga gaataaaata ataaaataaaa gtgtgatgtt acggtagacc 1321
171 ctttttttttt tttcttcatt tacggtagac ctatagtatt aaaacaaata gaatcagctg 1381
173 gttcggacct tgaaatgaga gagcttggat gcatgtagac gcattagtcg tgaattattc 1441
175 aaatagaact accttttggg ccaaaaaaaaa aaaaa 1476
178 <210> SEQ ID NO: 3
179 <211> LENGTH: 389
180 <212> TYPE: PRT
181 <213> ORGANISM: Arabidopsis thaliana
183 <400> SEQUENCE: 3
184 Met Glu Val Met Arg Val Leu His Met Asn Lys Gly Asn Gly Glu Thr
185 1 5 10 15
187 Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile Ile Ser Leu Gly
188 20 25 30

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190 Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met Met Ser Asn Ser
191          35          40          45
193 Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
194          50          55          60
196 Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr Ile His Asn Leu
197 65          70          75          80
199 Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg Val Ser Leu Asn
200          85          90          95
202 Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala Ser Leu Pro Glu
203          100          105          110
205 Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu Gly Phe Gly Arg
206          115          120          125
208 Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro Gly Ser Phe Tyr
209          130          135          140
211 Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val His Ser Ser Ser
212 145          150          155          160
214 Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu Ala Glu Lys Glu
215          165          170          175
217 Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly Lys Ile Tyr Ile
218          180          185          190
220 Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr Ala Leu Gln Phe
221          195          200          205
223 Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser Glu Glu Leu Val
224          210          215          220
226 Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg Arg Ser Leu Asp
227 225          230          235          240
229 Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu Leu Ala Gln Ala
230          245          250          255
232 Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu Glu Lys Ile Asp
233          260          265          270
235 Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu Glu Leu Lys Met
236          275          280          285
238 Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg Leu Glu Ile Ser
239          290          295          300
241 Pro Ile Asp Trp Glu Gly Ser Ile Ser Glu Glu Ser Tyr Asp Leu
242 305          310          315          320
244 Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly Arg Arg Val Ser
245          325          330          335
247 Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu Pro Thr Phe Gly
248          340          345          350
250 Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala Lys Ile Val Gly
251          355          360          365
253 Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile Val Ile Leu Ser
254          370          375          380
256 Leu Val Arg Thr Gly
257 385
260 <210> SEQ ID NO: 4
261 <211> LENGTH: 30
262 <212> TYPE: DNA

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10749187.061302

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263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence: 5' primer for
267     PCR of JMT gene
269 <400> SEQUENCE: 4
270 cgcgtccgaa ttcgagagag agagaatgga                                30
273 <210> SEQ ID NO: 5
274 <211> LENGTH: 30
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Description of Artificial Sequence: 3' primer for
280     PCR of JMT gene
282 <400> SEQUENCE: 5
283 tttgaagaat tcacgactaa tgcgtctaca                                30
286 <210> SEQ ID NO: 6
287 <211> LENGTH: 359
288 <212> TYPE: PRT
289 <213> ORGANISM: Clarkia breweri
291 <400> SEQUENCE: 6
292 Met Asp Val Arg Gln Val Leu His Met Lys Gly Gly Ala Gly Glu Asn
293   1           5           10           15
295 Ser Tyr Ala Met Asn Ser Phe Ile Gln Arg Gln Val Ile Ser Ile Thr
296           20           25           30
298 Lys Pro Ile Thr Glu Ala Ala Ile Thr Ala Leu Tyr Ser Gly Asp Thr
299           35           40           45
301 Val Thr Thr Arg Leu Ala Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
302           50           55           60
304 Asn Ala Leu Phe Ala Val Thr Glu Leu Ile Lys Thr Val Glu Glu Leu
305   65           70           75           80
307 Arg Lys Lys Met Gly Arg Glu Asn Ser Pro Glu Tyr Gln Ile Phe Leu
308           85           90           95
310 Asn Asp Leu Pro Gly Asn Asp Phe Asn Ala Ile Phe Arg Ser Leu Pro
311           100          105          110
313 Ile Glu Asn Asp Val Asp Gly Val Cys Phe Ile Asn Gly Val Pro Gly
314           115          120          125
316 Ser Phe Tyr Gly Arg Leu Phe Pro Arg Asn Thr Leu His Phe Ile His
317           130          135          140
319 Ser Ser Tyr Ser Leu Met Trp Leu Ser Gln Val Pro Ile Gly Ile Glu
320 145           150          155          160
322 Ser Asn Lys Gly Asn Ile Tyr Met Ala Asn Thr Cys Pro Gln Ser Val
323           165          170          175
325 Leu Asn Ala Tyr Tyr Lys Gln Phe Gln Glu Asp His Ala Leu Phe Leu
326           180          185          190
328 Arg Cys Arg Ala Gln Glu Val Val Pro Gly Gly Arg Met Val Leu Thr
329           195          200          205
331 Ile Leu Gly Arg Arg Ser Glu Asp Arg Ala Ser Thr Glu Cys Cys Leu
332           210          215          220
334 Ile Trp Gln Leu Leu Ala Met Ala Leu Asn Gln Met Val Ser Glu Gly

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107 9187 .051302

## VERIFICATION SUMMARY

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